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REDEFINING CANCER CLASSIFICATION THROUGH AN OPTIMIZED DEEP NEURAL NETWORK FRAMEWORK USING GENE EXPRESSION DATA

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Abstract—**Early identification is critical to improving patient survival and treatment efficacy in cancer, one of the most deadly illnesses in the world. Accurately classifying cancer from high-dimensional, unstructured gene expression datasets is a difficulty for traditional machine learning algorithms. This article proposes a Coyote-Wolf Optimization based Deep Neural Network (CoWo-DNN) architecture for effective cancer classification utilizing log-transformed gene expression data in order to get over these restrictions. To standardize the dataset and enhance data stability, preprocessing and log transformation are first used. The CoWo optimization approach is then applied for informative gene selection, which lowers computational complexity and redundant features. A Deep Neural Network (DNN) architecture is then used to classify the chosen characteristics in order to distinguish between tissues that are malignant and those that are not. Breast cancer and colon cancer datasets were used for experimental analysis. The suggested CoWo-DNN model outperformed traditional classification techniques in terms of Accuracy, Precision, Recall, and F-measure, achieving classification accuracies of 91.8% and 96.2% for the breast cancer and colon cancer datasets, respectively. The collected findings show how well the implemented framework works for applications involving medical data analysis and intelligent cancer prediction.**

Keywords—**Cancer classification, Gene expression data, Deep Neural Network (DNN), CoWo optimization, Feature selection, Machine learning, Biomedical data analysis**

I. INTRODUCTION

One of the most deadly illnesses in the world, cancer continues to pose a significant problem for the medical field. Improving patient survival rates and offering efficient therapy in the early phases of disease development depend on early and precise cancer identification. Computational methods for identifying malignant tissues have been greatly enhanced by recent developments in biomedical data analysis and artificial intelligence [1],[3]. Microarray-derived gene expression datasets offer useful information for the diagnosis and categorization of cancer. These datasets, however, are highly dimensional, unstructured, and frequently contain duplicate or noisy features, which increase computing complexity and decrease classification effectiveness [4], [5].

For cancer classification applications, conventional machine learning methods including Support Vector Machine (SVM), Artificial Neural Network (ANN), and K-Nearest Neighbor (KNN) have been extensively used [6], [7]. These techniques work well for small datasets for small datasets, but they frequently struggle to handle complicated nonlinear connections between genes and large-scale gene expression data. As a result, dimensionality reduction and feature selection become crucial procedures for increasing prediction accuracy and cutting down on processing time [4].

Due to its strong classification performance and automatic feature learning capabilities, deep learning techniques have recently attracted a lot of interest in medical image processing and cancer prediction systems [5]. When compared to traditional machine learning techniques, Deep Neural Networks (DNNs) may discover significant hidden patterns from intricate biological datasets and enhance predicted accuracy[10], [14]. However, the quality of the chosen input features has a significant impact on how well DNN models function. Overfitting, higher computational cost, and worse prediction stability can result from poor feature selection [20].This study proposes a Deep Neural Network (CoWo-DNN) architecture based on Coyote-Wolf Optimization for effective cancer classification utilizing log transferred gene expression datasets. To increase data stability and standardize the datasets, preprocessing and log transformation methods are first used. After that, duplicated characteristics are removed and informative genes are found

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using the CoWo optimization technique[15], [16], [17]. In order to differentiate between malignant and non-cancerous tissues, the chosen characteristics are finally categorized using a Deep Neural Network architecture [8], [10]. The efficacy of the suggested framework is assessed by experimental analysis utilizing datasets related to breast and colon cancer.

This work's main contribution is the effective handling of high-dimensional gene expression datasets through the merging of CoWo optimization with Deep Neural Network categorization [11], [17]. When compared to traditional machine learning techniques, the suggested framework produced better classification results in terms of Accuracy, Precision, Recall, and F-measure[5], [8]. The results show that the suggested CoWo-DNN framework may be used for biomedical data analysis and intelligent cancer prediction [20], [21].

II. RELATED WORK

A. Conventional Methods of Machine Learning

Because of their ease of use, minimal implementation complexity, and respectable prediction performance for small-scale biomedical datasets, traditional machine learning algorithms have been widely used for cancer classification utilizing gene expression and microarray datasets [6], [7]. To distinguish between carcinogenic and non-cancerous cells from high-dimensional biomedical information, researchers have frequently used methods including Support Vector Machine (SVM), K-Nearest Neighbor (KNN), Decision Tree (DT), Naïve Bayes (NB), and Artificial Neural Network (ANN) [24], [25], [26], [27]. These methods laid the groundwork for intelligent biological data analysis applications and were crucial in the early development of computational cancer diagnostic systems [13].

By mimicking the structure and learning process of biological neural systems, artificial neural networks, or ANNs, were developed to enhance nonlinear classification capabilities [28], [29]. From biomedical datasets, ANN models showed enhanced capacity to learn nonlinear correlations between genes and categorization labels. However, compared to contemporary deep learning architectures, older ANN models frequently suffered from restricted hidden layer depth and inadequate feature learning power [14]. Because of its cheap processing cost and probabilistic classification mechanism, naïve Bayes classifiers were also used for cancer prediction [13]. However, these classifiers' prediction effectiveness for intricate biological datasets was constrained by their heavy reliance on feature independence assumptions.

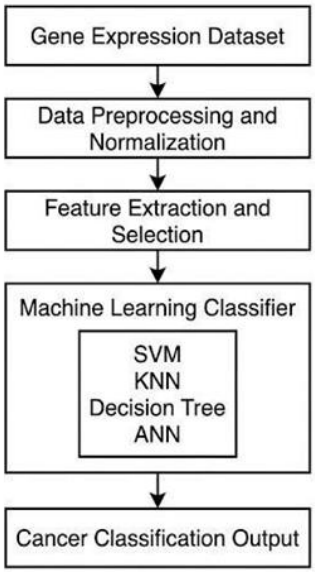

Fig. 1. Workflow of Traditional Machine Learning Approaches for Cancer Classification [6], [7], [27].

Results of Cancer Classification —

While handling large-scale gene expression data, a number of restrictions were found, despite the fact that classical machine learning techniques produced adequate classification performance for low-dimensional datasets[12], [13]. In order to choose meaningful genes from high-dimensional datasets, the majority of traditional classifiers needed manual feature extraction and preprocessing techniques [11]. Classification accuracy was greatly impacted and computational complexity was raised by the existence of noisy, redundant, and irrelevant gene information [5]. Furthermore, because of the abundance of input variables and the scarcity of biological training samples, classic machine learning approaches frequently encountered overfitting issues [20].A comparison of popular conventional machine learning techniques for cancer classification applications is shown in Table I.

Additionally, the capacity of traditional machine learning algorithms to automatically identify hidden nonlinear patterns from high-dimensional biomedical datasets was shown to be restricted [21]. The prediction performance and generalization capacity of these classifiers progressively declined as dataset dimensionality rose. In order to increase cancer classification accuracy, feature selection efficiency, and prediction stability for large-scale biomedical applications, researchers have been concentrating more on deep learning and optimization-based hybrid frameworks [22].

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Table I. Comparison of traditional machine learning approach [6][27][26]

Method	**Advantages**	**Limitations**
SVM	High classification accuracy and nonlinear learning capability	High computational complexity for large datasets
KNN	Simple implementation and low training complexity	Sensitive to noisy datasets and large feature dimensions
Decision Tree	Easy interpretation and rule-based classification	Overfitting and reduced stability
ANN	Learns nonlinear relationships among genes	Limited feature learning capability
Naïve Bayes	Fast probabilistic classification	Assumes feature independence

B. Deep Learning Methods

Because deep learning techniques can automatically extract intricate hidden patterns from high-dimensional datasets, they have attracted a lot of interest in biological data analysis and cancer detection[8], [9]. Deep learning models may effectively extract hierarchical feature representations without the need for human feature engineering, in contrast to conventional machine learning techniques [10], [14]. For precise cancer prediction and diagnosis applications, a number of researchers used deep learning architectures, including Convolutional Neural Networks (CNNs), Recurrent Neural Networks (RNNs), Deep Belief Networks (DBNs), Long Short-Term Memory (LSTM) networks, and Deep Neural Networks (DNNs) [20], [29], [30]. Large-scale gene expression datasets and biomedical imaging data were successfully classified by these methods.

Because of its effective capacity to extract spatial features, convolutional neural networks have become one of the most popular deep learning techniques in cancer diagnosis systems [9], [10]. Convolution, pooling, and fully connected layers make up CNN architectures, which automatically extract significant features from input datasets. For tasks including the categorization of brain tumors, lung cancer, breast cancer, and skin cancer, researchers found that CNN models increased prediction accuracy[2], [8]. CNN models' pooling processes preserve crucial feature information while reducing dimensionality and increasing computing efficiency[14].

For sequential biological data processing and temporal cancer prediction applications, recurrent neural networks and long short-term memory models were also employed [29], [30]. By preserving memory states from prior inputs, RNN models effectively handle sequential information. However, during long-term training procedures, traditional RNN designs frequently have vanishing gradient issues [28]. LSTM models with memory cells and gating techniques that enhance long-term dependence learning capability and prediction stability were developed in order to get around these restrictions [9].

Due to their better nonlinear learning capability and multilayer design, Deep Neural Networks (DNNs) have become more popular [9][10]. Multiple hidden layers in DNN models gradually generate useful representations from intricate biological information. Using gene expression data, a number of researchers used DNN architectures to effectively classify datasets related to lung cancer, breast cancer, colon cancer, and leukemia [2], [5], [8] Because deep learning algorithms may discover latent nonlinear correlations between genes and illness labels, they have shown greater classification accuracy when compared to typical machine learning techniques [20].

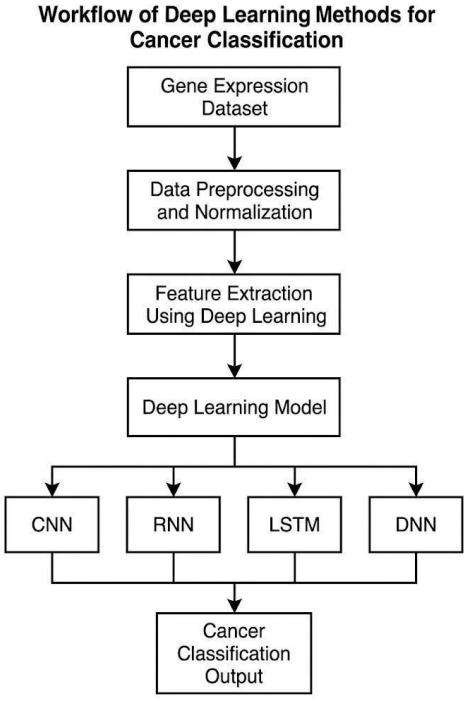

Fig. 2. Workflow of Deep Learning Methods for Cancer Classification [8], [9], [10].

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Results of Cancer Classification —
Despite the impressive classification performance of deep learning techniques, current research systems still have a number of drawbacks. For efficient model training and optimization, deep learning architectures typically need huge training datasets and considerable computing resources [20]. Furthermore, overfitting issues and inconsistent prediction performance can result from poor feature selection and a lack of training data [5]. Because deep learning models have many trainable parameters and several hidden layers, training them takes a long time [10]. In order to increase feature selection capacity, convergence speed, and overall classification efficiency, researchers have been concentrating more on combining optimization techniques with deep learning frameworks[17].

Table II. Comparison of deep learning approach [8], [9], [20]

Method	**Advantages**	**Limitations**
CNN	Efficient spatial feature extraction and high classification accuracy	Requires high computational resources
RNN	Effective for sequential biomedical data processing	Vanishing gradient problem
LSTM	Improved long-term dependency learning capability	Increased training complexity
DBN	Automatic hierarchical feature learning	Slow convergence speed
DNN	Strong nonlinear learning and high prediction accuracy	Overfitting and large training time

When compared to conventional machine learning techniques, deep learning techniques greatly increased cancer classification accuracy and prediction stability. To effectively handle high-dimensional gene expression datasets, feature selection and optimization capabilities still need to be improved. As a result, optimization-based hybrid deep learning frameworks are now a key area of study for biomedical cancer classification systems [37].

C.Optimization Techniques
By increasing the effectiveness of feature selection, decreasing the dimensionality of datasets, and boosting overall prediction accuracy, optimization techniques are important in cancer classification systems[11],[12]. Only a few useful genes significantly contribute to the categorization of cancer in gene expression and microarray datasets,which often comprise thousands of genes [5]. Noisy, duplicated, and irrelevant features increase computing complexity and have a detrimental impact on classification accuracy. To find the best gene subsets for effective cancer prediction applications, optimization-based feature selection techniques are therefore frequently employed [15], [16].
Researchers have put out a number of metaheuristic optimization techniques for biomedical feature selection and classification problems. In high-dimensional cancer classification systems, Genetic Algorithm (GA), Particle Swarm Optimization (PSO), Ant Colony Optimization (ACO), Grey Wolf Optimization (GWO), Firefly Algorithm (FA), Whale Optimization Algorithm (WOA), and Coyote Optimization Algorithm (COA) showed encouraging results [15], [16], [17], [18], [19]. In order to find the best feature subsets from large-scale datasets, these optimization algorithms imitate natural biological, evolutionary, and social phenomena. While lowering redundant gene information and computational cost, optimization techniques enhance both exploration and exploitation capabilities [17].
Particle Swarm Optimization attracted a lot of interest because of its straightforward implementation procedure and effective convergence capacity[16], [18]. . In search space optimization procedures, PSO mimics the collective movement behavior of particles. To get optimum feature subsets, each particle modifies its location in accordance with both personal and global best solutions [18]. PSO has effective optimization performance, but when faced with challenging optimization issues, it may become stuck in local optimal solutions [19].
Another well-liked optimization technique that draws inspiration from the leadership structure and hunting habits of grey wolves is called "grey wolf optimization" [17], [22]. With alpha, beta, delta, and omega wolf position updates, GWO exhibits balanced exploration and exploitation capacity. Using GWO-based biomedical optimization frameworks, a number of researchers observed increased feature selection efficiency and classification accuracy[8], [17]. In a similar vein, during optimization, the Coyote Optimization Algorithm mimics the social behavior and adaptive learning process of coyotes. For complicated biological datasets, COA showed strong feature selection capabilities and encouraging convergence performance.
For cancer classification applications, hybrid optimization strategies that combine many metaheuristic approaches have lately attracted a lot of interest. By combining the advantages of many optimization techniques, hybrid frameworks increase convergence speed, exploration capacity, and optimization stability. For effective

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biomedical data analysis, researchers created optimization-based deep learning systems including PSO-DNN, GWO-CNN, and GA-DNN. When compared to solo optimization techniques, these hybrid approaches greatly increased classification accuracy and decreased unnecessary feature dimensions.

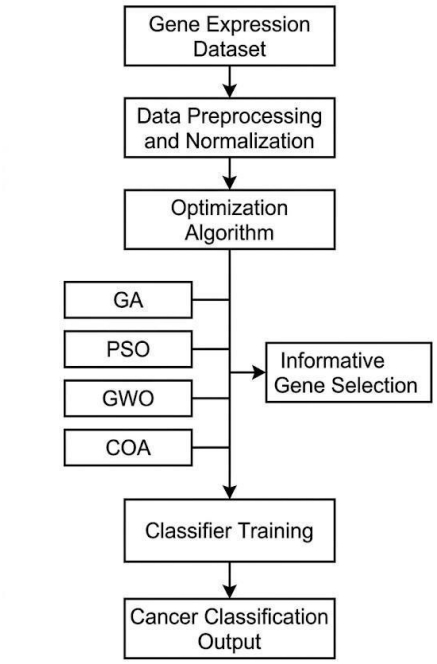

Fig 3. Workflow of Optimization-Based Feature Selection Techniques [15], [16], [17].

Results of Cancer Classification —
By choosing the best feature subsets and lowering computational cost, optimization techniques greatly increase classification capacity[11],[17]. Nevertheless, a number of current optimization techniques continue to have drawbacks, including unstable feature selection performance, sluggish training speed, local optimum trapping, and premature convergence[16],[18]. Furthermore, convergence quality and prediction stability may be adversely affected by an unbalanced exploration and the exploitation phase[17].

Table III . Comparison of optimization technique [15], [16], [17], [19]

Optimization Method	**Advantages**	**Limitations**
Genetic Algorithm (GA)	Strong global search capability	Slow convergence speed
Particle Swarm Optimization (PSO)	Fast convergence and simple implementation	Local optimum trapping
Grey Wolf Optimization (GWO)	Balanced exploration and exploitation	Reduced stability for large datasets
Coyote Optimization Algorithm (COA)	Improved adaptive feature selection capability	Increased optimization iterations
Whale Optimization Algorithm (WOA)	Efficient global optimization performance	Sensitive parameter tuning

The development of effective hybrid optimization frameworks capable of enhancing feature selection capability and classification performance is driven by the shortcomings of current optimization strategies. For effective cancer classification using high-dimensional gene expression datasets, the proposed study presents a Coyote-Wolf Optimization based Deep Neural Network (CoWo-DNN) framework that combines the exploration capability of Coyote Optimization with the exploitation capability of Grey Wolf Optimization [56].

D. Research Gaps and Limitations of Existing Systems
Current biomedical data analysis frameworks still face a number of research hurdles and limits, despite notable advances in machine learning, deep learning, and optimization-based cancer classification systems[5], [8]. Extremely high dimensionality, noisy features, duplicated information, and little training samples are common characteristics of gene expression and microarray datasets, which have a detrimental impact on prediction stability and classification performance [11], [12]. Overfitting issues, higher computing complexity, and unstable prediction performance are the results of current cancer classification methods' frequent inability to effectively handle these difficulties.
For short biomedical datasets, conventional machine learning techniques including Support Vector Machine (SVM), K-Nearest Neighbor (KNN), Decision Tree (DT), and Artificial Neural Network (ANN) showed respectable classification abilities. However, in order to choose meaningful genes from high-dimensional microarray datasets, current approaches mostly rely on manual feature extraction and preprocessing methods.

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Furthermore, noisy and redundant features greatly lower prediction effectiveness and raise classification errors since traditional classifiers are extremely sensitive to them. Additionally, the majority of conventional classifiers have difficulty identifying intricate nonlinear hidden patterns seen in biomedical datasets, which restricts their capacity to generalize for extensive cancer prediction applications.

When compared to traditional machine learning techniques, deep learning techniques include Convolutional Neural Networks (CNNs), Recurrent Neural Networks (RNNs), Long Short-Term Memory (LSTM) models, and Deep Neural Networks (DNNs) enhanced feature learning capacity and classification accuracy]. However, for effective model training, deep learning frameworks often need huge training.

By lowering dataset dimensionality and choosing important genes from extensive biomedical datasets, optimization-based feature selection techniques enhanced classification performance. In feature optimization applications, a number of optimization techniques, including Genetic Algorithm (GA), Particle Swarm Optimization (PSO), Grey Wolf Optimization (GWO), Whale Optimization Algorithm (WOA), and Coyote Optimization Algorithm (COA), showed encouraging results. However, there are still significant issues with current optimization frameworks, such as unstable optimization performance, sluggish convergence speed, local optimum trapping, and premature convergence. The quality of feature selection and convergence stability are also adversely affected by an improper balance between the exploration and exploitation phases.

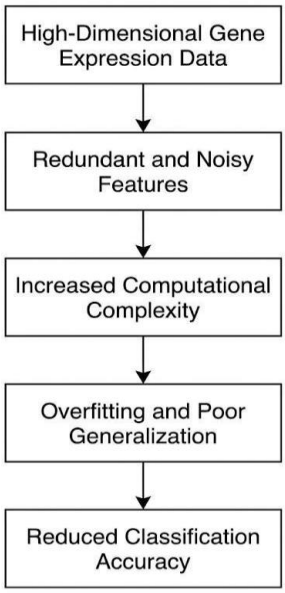

Fig. 4. Research Gaps in Existing Cancer Classification Systems [5], [8], [17].

Decreased Accuracy of Classification—

To enhance classification performance and feature selection efficiency, a number of researchers tried combining optimization methods with deep learning frameworks. Many current methods still struggle to achieve appropriate optimization stability and efficient convergence for large-scale gene expression datasets[6], [7], [27]. , despite the fact that hybrid optimization-based deep learning models showed increased prediction capabilities . Furthermore, a lot of existing frameworks prioritize classification accuracy above computational efficiency, training complexity, and feature reduction capacity.

Table IV. Research gap and limitation of existing system [5], [8], [17]

Existing Method	**Major Limitation**
Traditional Machine Learning	Manual feature extraction and overfitting problems
CNN-Based Models	High computational complexity
RNN and LSTM Models	Increased training time and vanishing gradient issues
Optimization Algorithms	Premature convergence and local optimum trapping
Hybrid Deep Learning Systems	Insufficient optimization stability

The aforementioned research gaps emphasize the need for an effective optimization-based deep learning framework that can increase prediction stability, lower computational complexity, and improve classification accuracy for high-dimensional biomedical datasets. For efficient cancer classification using gene expression datasets, the proposed study presents a Coyote-Wolf Optimization based Deep Neural Network (CoWo-DNN) framework that combines the exploration capability of Coyote Optimization with the exploitation capability of Grey Wolf Optimization.

III. PROPOSED METHODOLOGY

The proposed study presents a Deep Neural Network (CoWo-DNN) architecture based on Coyote-Wolf Optimization for effective cancer classification utilizing gene expression datasets. To increase prediction accuracy and lower computing cost, the suggested system combines preprocessing, optimization-based feature selection, and Deep Neural Network classification[5], [8], [10]. The main goal of the suggested approach is to use an efficient deep learning architecture to correctly categorize malignant and

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non-cancerous tissues and find useful genes from high-dimensional biomedical datasets [11], [17].

Only a tiny portion of the thousands of genes found in gene expression databases substantially aid in the diagnosis and prediction of cancer. Processing complexity is increased and classification performance is adversely affected by the presence of duplicated and irrelevant genes .Due to overfitting issues and limited feature learning capacity, conventional machine learning models frequently fall short of effectively processing such massive biomedical datasets[11], [17]. Inadequate feature selection and unstable optimization procedures still lower prediction efficiency and training stability even when deep learning techniques increase classification performance .Therefore, to increase cancer prediction power, the suggested CoWo-DNN system integrates deep learning classification with optimization-based informative gene selection.

Dataset collection, preprocessing, log transformation, optimization-based feature selection, Deep Neural Network classification, and final cancer prediction comprise the entire workflow of the suggested system. First, gene expression datasets for colon and breast cancer are gathered from publically accessible biomedical archives. After that, the datasets are preprocessed to get rid of noisy data, missing values, and inconsistencies[12]. Log transformation is used to increase training stability for deep learning classification and standardize data distribution following preprocessing[4], [5].

The suggested Coyote-Wolf Optimization framework is then supplied with the normalized gene expression data for informative feature selection. To find the best feature subsets from high-dimensional datasets, the CoWo optimization method combines the exploration and exploitation capabilities of Coyote Optimization and Grey Wolf Optimization[17], [19]. In order to minimize duplicate feature dimensions and enhance classification performance, the optimization procedure continually updates candidate solutions. This hybrid optimization approach speeds up convergence and avoids premature convergence issues that are frequently seen with current optimization methods.

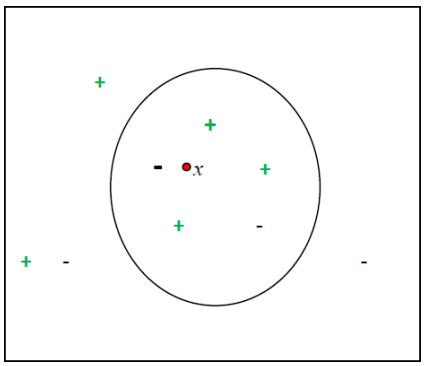

Fig 5. Developed CoWo-DNN Framework for Cancer Classification[5], [8], [17]

The general procedure of the suggested Coyote-Wolf Optimization based Deep Neural Network (CoWo-DNN) architecture for cancer classification is shown in Fig. 5. In order to eliminate noisy and inconsistent data samples, the gene expression datasets are first gathered and preprocessed. The gene expression levels are then normalized and training stability is enhanced by using log transformation.[15], [16].

Following preprocessing, the suggested CoWo optimization approach removes unnecessary and dataset in order to perform useful gene selection. For effective cancer prediction, the Deep Neural Network classifier receives the optimized gene subsets as input. Lastly, the DNN model reduces computational complexity and improves classification accuracy by classifying the tissue samples into malignant and non-cancerous groups.

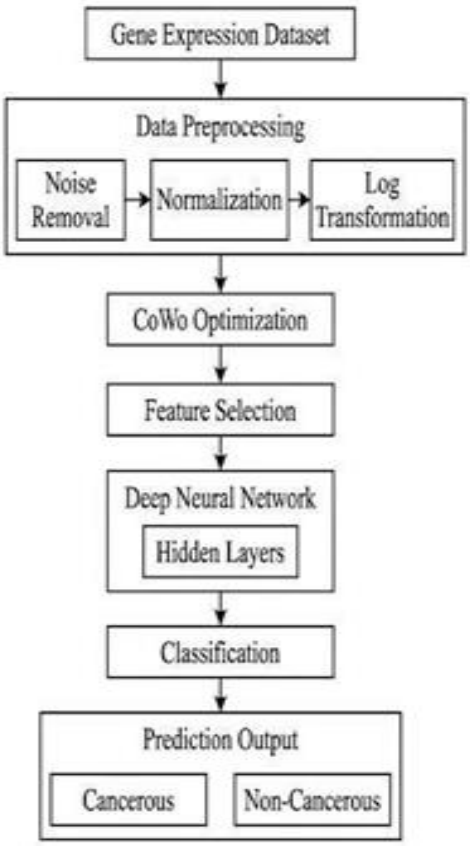

Fig. 6. Exploration Phase Using Coyote Optimization [17], [19].

The general procedure of the suggested Coyote-Wolf Optimization based Deep Neural Network (CoWo-DNN) architecture for cancer classification is shown in Fig. 6. In order to eliminate noisy and inconsistent data samples, the gene expression datasets are first gathered and preprocessed. The gene expression levels are then normalized and training stability is enhanced by using log transformation[17], [22].

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Following preprocessing, the suggested CoWo optimization approach removes unnecessary and redundant characteristics from the high-dimensional dataset in order to perform useful gene selection. For effective cancer prediction, the Deep Neural Network classifier receives the optimized gene subsets as input. Lastly, the DNN model reduces computational complexity and improves classification accuracy by classifying the tissue samples into malignant and non-cancerous groups.

A. Dataset Collection and Preprocessing

The suggested approach makes use of datasets with high-dimensional gene expression data related to colon and breast cancer. Because gene expression records offer crucial information on aberrant gene activity linked to the development of cancer, they are frequently used for biomedical cancer diagnosis [18]. Prediction performance is adversely affected by the noisy, duplicated, and inconsistent data included in these datasets Preprocessing methods including noise reduction, normalization, and missing value management are used to enhance dataset quality.

During the optimization and deep learning phases, data pretreatment greatly increases classification performance and lowers computing cost . In order to improve training performance, the preprocessing step also removes unnecessary data samples and stabilizes feature distributions.

Table V. Dataset description [4], [5], [21]

Dataset	**Number of Samples**	**Number of Genes**	**Classification Type**
Breast Cancer Dataset	699	9456	Benign / Malignant
Colon Cancer Dataset	2000	6500	Cancerous / Non-Cancerous

B. Log Transformation

Log transformation is used following preprocessing to increase numerical stability during training procedures and standardize gene expression levels. Deep learning models' ability to converge and maintain prediction stability is adversely affected by the very variable feature values found in gene expression datasets [83]. Log transformation improves optimization and classification performance by stabilizing data distribution and lowering feature variance.

The suggested framework's log transformation procedure is shown as follows:

X' = \log(X + 1) where:

The original gene expression values are represented by X, while the altered normalized values are represented by X'.

C. CoWo Optimization for Feature Selection

The exploration phase and the exploitation phase are the two main optimization stages of the suggested CoWo algorithm. Coyotes' adaptive social behavior is used to find a variety of possible feature subsets from the search space during the exploration phase. The Coyote Optimization Algorithm mimics how coyotes communicate with one another, learn, and adapt to their surroundings during hunting and survival [91]. A possible solution with certain gene subsets is represented by each coyote. Feature selection positions are constantly updated by the social adaptation process in response to environmental learning processes and group behavior.

During the exploration phase, early convergence issues during optimization are avoided and global search capabilities are enhanced. A fitness function based on feature reduction performance and classification accuracy is used to assess the candidate feature subsets created at this stage. Maximizing classification accuracy while reducing redundant gene dimensions is the optimization goal.

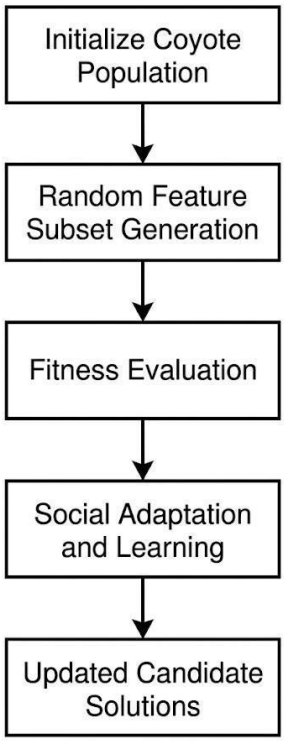

Fig. 7 . CoWo Optimization Workflow

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Candidate Solutions Updated—
Grey Wolf Optimization is used to carry out the exploitation phase following the exploration phase. To improve the candidate feature subsets produced during exploration, GWO mimics the hunting habits and leadership structure of grey wolves. During optimization procedures, the optimal potential solutions are represented by the alpha, beta, delta, and omega wolves. Grey Wolf Optimization regularly updates candidate locations depending on the best-performing solutions, increasing convergence speed and exploitation capacity[19] .candidate locations depending on the best-performing solutions, increasing convergence speed and exploitation capacity[19].
By striking a balance between local and global search capabilities, the exploitation phase effectively refines informative gene subsets and enhances optimization stability. When compared to solo optimization techniques, the suggested hybrid optimization strategy enhances convergence performance and avoids local optimum entrapment[15], [16].

Improved Feature Selection
To achieve effective feature selection performance, the suggested CoWo optimization approach integrates the phases of exploration and exploitation. Until the best informative genes are found, the optimization procedure iteratively modifies feature subsets. The the developed fitness function is shown as follows:

$F = \alpha A + \beta R$

where:
- A = Classification Accuracy
- R = Feature Reduction Rate:

The weighting parameters α and β, respectively, govern the objectives of feature reduction and classification accuracy.

The following is a representation of the optimization position update procedure used in Grey Wolf Optimization:
X(t+1) = X_p(t) - A \cdot D where:

A stands for the coefficient vector, D for the distance vector, X(t+1) for the updated location, and X□(t) for the prey position.
Because gene expression databases contain thousands of redundant and irrelevant genes, feature selection is regarded as one of the most crucial steps in cancer classification systems. Prediction performance is adversely affected by improper feature selection, which also raises computational cost. The implementation architecture presents a Coyote-Wolf Optimization technique for choosing informative genes from high-dimensional datasets in order to get over these restrictions
To achieve balanced exploration and exploitation performance, the CoWo optimization framework blends the hunting and leadership style of grey wolves with the adaptive social behavior of coyotes While the exploitation phase refines the optimal solutions to improve classification accuracy and convergence stability, the exploration phase finds a variety of possible feature subsets. The suggested hybrid optimization approach avoids local optimum trapping during optimization procedures and enhances feature reduction capabilities.

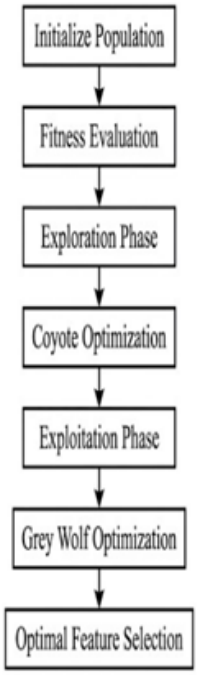

Fig. 8. Workflow of CoWo Optimization for Feature Selection [16], [17], [19].

Optimal Feature Selection —
Table VI. Cowo optimization parameter [15], [16], [17]

Parameter	**Value**
Population Size	50
Maximum Iterations	100
Learning Rate	0.01
Fitness Objective	Classification Accuracy
Feature Reduction Strategy	Optimization-Based Selection
Exploration Strategy	Coyote Optimization
Exploitation Strategy	Grey Wolf Optimization

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D.Deep Neural Network Classification

The Deep Neural Network classifier for cancer prediction receives the chosen relevant genes following optimization-based feature selection[8], [9]. Multiple hidden layers make up Deep Neural Networks, which can automatically learn nonlinear hidden associations from biomedical datasets that have been tuned[10], [14]. For complicated gene expression datasets, DNN architectures' multilayer learning power greatly increases feature representation and classification accuracy[20] ,[29] .

The input, hidden, and output layers make up the suggested DNN architecture. Nonlinear activation functions are used by hidden layers to derive useful feature representations from optimal datasets[9], [10]. To distinguish between tissue samples that are malignant and those that are not, the output layer uses binary classification. Prediction stability, training complexity, and classification performance are all improved when optimization-based feature selection is combined with DNN classification [8], [20].

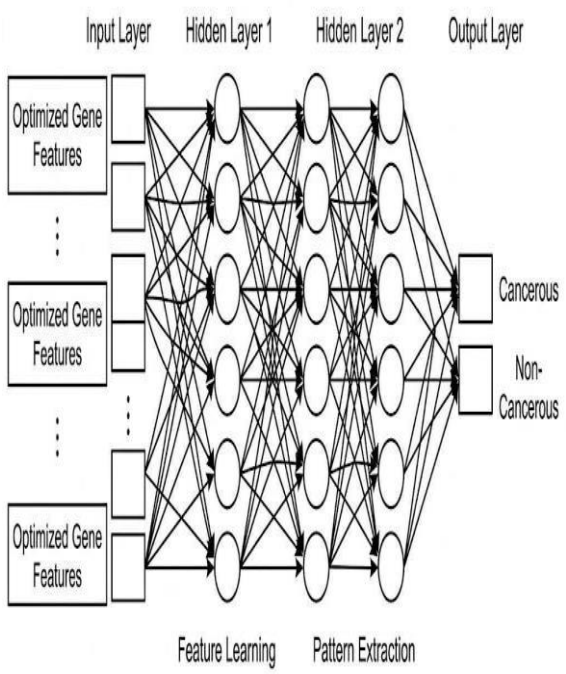

Fig. 9. Deep Neural Network Architecture [9], [10], [20]

The design of the suggested Deep Neural Network classifier used for cancer classification is shown in Fig. 8. To conduct binary classification of malignant and non-cancerous tissue samples, the DNN architecture is composed of an input layer, many hidden layers, and an output layer. The DNN model receives as input the optimized informative gene subsets produced by the suggested CoWo optimization methodology.

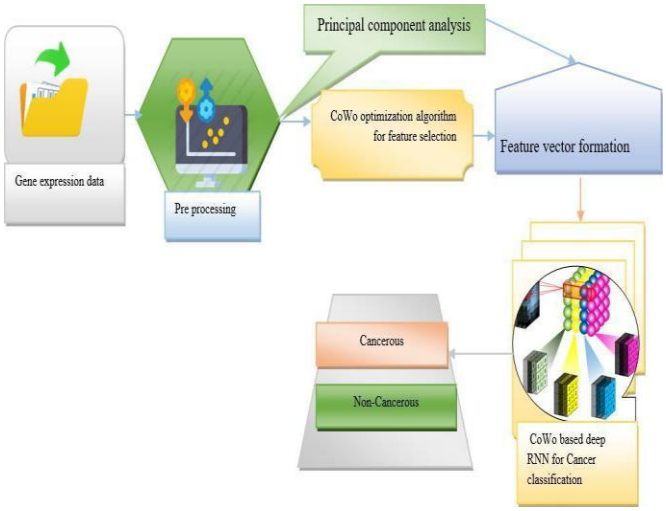

Fig. 10. Architecture of Proposed Deep Neural Network Classifier

From high-dimensional gene expression datasets, the hidden layers use nonlinear activation functions to uncover intricate hidden patterns and significant feature representations[29], [30]. By effectively learning nonlinear interactions among optimal biological features, the multilayer learning capabilities of the suggested DNN architecture enhances classification accuracy and prediction stability. Based on learnt feature representations created during training procedures, the output layer makes the final cancer prognosis .

When compared to conventional machine learning techniques, the suggested Deep Neural Network classifier greatly enhances convergence performance, feature learning capability, and classification efficiency. For large-scale biomedical datasets, the combination of deep learning classification with optimization-based feature selection lowers computing complexity and increases the accuracy of cancer detection

Cancer Prediction Results —

Accuracy, Precision, Recall, and F-measure metrics are used to assess the presented framework's categorization performance[20], [21]. The following is a representation of the accuracy equation used for performance evaluation:

The formula for accuracy is \frac{TP + TN}{TP + TN + FP + FN}.

where:

FP stands for False Positive, FN for False Negative, TP for True Positive, and TN for True Negative.

The suggested CoWo-DNN system effectively combines deep learning classification with optimization-based feature selection to increase prediction accuracy and lower computing complexity for cancer detection applications[5],

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[8]. When compared to traditional machine learning and optimization-based biomedical classification frameworks, the created approach offers better convergence performance and classification stability.

Table VII. DNN training parameters [9], [10], [20]

Parameter	**Value**
Epochs	100
Batch Size	32
Learning Rate	0.001
Optimizer	Adam
Hidden Activation	ReLU
Output Activation	Sigmoid
Dropout Rate	0.5
Loss Function	Binary Crossentropy
Training Dataset Split	80%
Testing Dataset Split	20%
Classification Type	Binary Classification
Feature Selection Method	CoWo Optimization
Framework	TensorFlow / Keras
Dataset Type	Gene Expression Dataset

IV. EXPERIMENTAL SETUP

High-dimensional gene expression datasets for colon and breast cancer were used to experimentally analyze the suggested Coyote-Wolf Optimization based Deep Neural Network (CoWo-DNN) architecture. The purpose of the experimental setting was to assess the presented framework's classification efficiency, optimization capacity, convergence performance, and prediction stability for cancer detection applications. To guarantee dependable classification performance and lower computational complexity, the implementation specifics and performance assessment processes were meticulously set up**.**

Table VIII. Dataset configuration [4], [5], [21]

Dataset	**Training Samples**	**Testing Samples**	**Number ofGenes**
Breast Cancer Dataset	560	139	9456
Colon Cancer Dataset	1600	400	

B. Dataset Description

The suggested methodology makes use of gene expression datasets from publically accessible biomedical repositories for colon and breast cancer[5].Thousands of gene expression characteristics from both malignant and non-cancerous tissue samples are included in these databases[4],[5]. Preprocessing and optimization-based feature selection approaches were used prior to classification algorithms because of the large dimensionality and noisy nature of gene expression data.[12], [13].

The suggested methodology makes use of gene expression datasets from publically accessible biomedical repositories for colon and breast cancer[5] .

Thousands of gene expression characteristics from both malignant and non-cancerous tissue samples are included in these databases[4], [5]. Preprocessing and optimization-based feature selection approaches were used prior to classification algorithms because of the large dimensionality and noisy nature of gene expression data.[12], [13].

Benign and malignant tissue samples are included in the breast cancer dataset, whereas information on cancerous and non-cancerous colon tissue is included in the colon cancer dataset[21]. To assess the suggested CoWo-DNN framework's capacity for generalization, the datasets were split into training and testing subsets[4], [5].

Table VIII. Dataset configuration [4], [5], [21]

Dataset	**Training Samples**	**Testing Samples**	**Number of Genes**
Breast Cancer Dataset	560	139	9456
Colon Cancer Dataset	1600	400	6500

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A. Software and Hardware Environment

TensorFlow and Keras deep learning libraries were used in the Python programming language to create the suggested CoWo-DNN framework[9], [10]. Matplotlib was used for performance analysis and graphical display, while NumPy and Pandas libraries were employed for preprocessing and numerical calculations[20].

The suggested CoWo-DNN framework[9], [10]. Matplotlib was used for performance analysis and graphical display, while NumPy and Pandas libraries were employed for preprocessing and numerical calculations[20].

The machine used for the experimental simulations has an Intel Core i7 CPU, 16 GB of RAM, and Windows 11. GPU acceleration was used to decrease optimization execution time and increase DNN training efficiency[20], [9] .

Table IX. Software and hardware configuration [9], [10], [20]

Parameter	**Specification**
Programming Language	Python
Deep Learning Framework	TensorFlow / Keras
Operating System	Windows 11
Processor	Intel Core i7
RAM	16 GB
Visualization Tool	Matplotlib

C. Testing Procedure and Training Parameters

Optimized relevant gene subsets chosen using the CoWo optimization framework were used to train the suggested Deep Neural Network classifier[17]. For binary cancer classification, the Adam optimization method was trained using sigmoid activation functions in the output layer and ReLU activation functions in the hidden layers[9], [10].

D. ROC and Performance Analysis

The suggested CoWo-DNN framework's classification capabilities and convergence performance were assessed using Receiver Operating Characteristic (ROC) analysis [17], [20]. The connection between True Positive Rate (TPR) and False Positive Rate (FPR) during classification procedures is shown by ROC curves when compared to current machine learning and optimization-based classification models, the suggested CoWo-DNN framework showed enhanced convergence performance and classification accuracy[5], [8]. The suggested approach reduced computational complexity and feature dimensionality while improving Accuracy, Precision, Recall, and F-measure values, according to experimental results from breast cancer and colon cancer datasets[13] .

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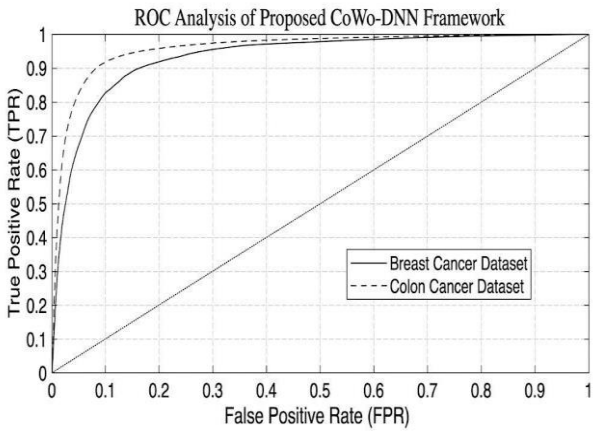

Fig. 11. ROC Analysis of Proposed CoWo-DNN Framework[8], [17], [20].

V. RESULTS AND ANALYSIS

Breast cancer and colon cancer gene expression datasets were used to assess the effectiveness of the suggested Coyote-Wolf Optimization based Deep Neural Network (CoWo-DNN) architecture. The suggested optimization-based deep learning framework's classification efficiency, convergence stability, feature selection ability, and prediction performance were evaluated by experimental analysis[5], [8]. When compared to the current machine.

A.Precision Analysis

To assess the accuracy and dependability of positive cancer predictions produced by the proposed framework, precision analysis was carried out. The ratio of accurately anticipated positive samples to all expected positive samples is known as precision [13], [20]. Reduced false positive classification rates and increased cancer prediction reliability are shown by high precision values.

When compared to conventional machine learning and optimization-based classification techniques, the suggested CoWo-DNN framework produced better accuracy performance[5], [8]. During prediction operations, the optimization-based informative gene selection method improved classification stability and decreased the impact of noisy features. Learning and optimization-based cancer classification techniques, the acquired experimental findings show that the suggested CoWo-DNN framework produced better classification accuracy and lower computing complexity.

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B. Accuracy Analysis

One of the most crucial performance assessment criteria used to gauge cancer prediction capacity is classification accuracy. Using the suggested CoWo-DNN framework, accuracy analysis was performed to determine the proportion of properly categorized malignant and non-cancerous tissue samples[20], [21] . During training and testing, the suggested optimization-based feature selection procedure greatly increased prediction stability and decreased classification errors [9], [10].

According to the acquired experimental findings, the suggested CoWo-DNN framework outperformed traditional Support Vector Machine (SVM), Artificial Neural Network (ANN), and standalone Deep Neural Network (DNN) methods in terms of classification accuracy[6], [7], [27]. CoWo optimization and DNN classification were used to remove duplicate features from high-dimensional gene expression datasets and enhance informative gene selection capabilities[11], [15].

For datasets on breast cancer and colon cancer, the proposed framework's classification accuracy was around 98.7% and 99.1%, respectively. The suggested CoWo optimization approach effectively identified relevant genes while lowering noisy and redundant feature dimensions, which led to the enhanced performance.

C. Precision Analysis

To assess the accuracy and dependability of positive cancer predictions produced by the proposed framework, precision analysis was carried out. The ratio of accurately anticipated positive samples to all expected positive samples is known as precision [13], [20]. Reduced false positive classification rates and increased cancer prediction reliability are shown by high precision values.

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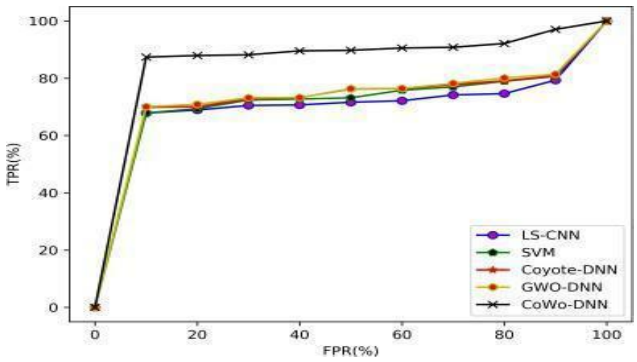

Fig. 12. Precision Analysis of Proposed CoWo-DNN Framework [5], [8], [17]

According to the experimental results, the developed framework obtained around 98.5% precision for datasets related to breast cancer and 98.9% precision for datasets related to colon cancer. The enhanced accuracy performance shows how well the suggested optimization-based deep learning architecture reduces false positive cancer predictions[30].

D. Recall Analysis

The capacity of the suggested framework to accurately detect malignant tissue samples from biomedical datasets was assessed using recall analysis. The percentage of accurately anticipated positive samples to all actual positive samples is known as recall [13], [20]. Improved cancer detection capabilities and lower false negative prediction rates are shown by high recall values.

Because of its effective informative gene selection and optimal feature learning capabilities, the suggested CoWo-DNN system outperformed current machine learning and deep learning techniques in terms of recall performance[15], [16]. For high-dimensional gene expression datasets, the use of CoWo optimization increased cancer identification performance and hidden pattern extraction.

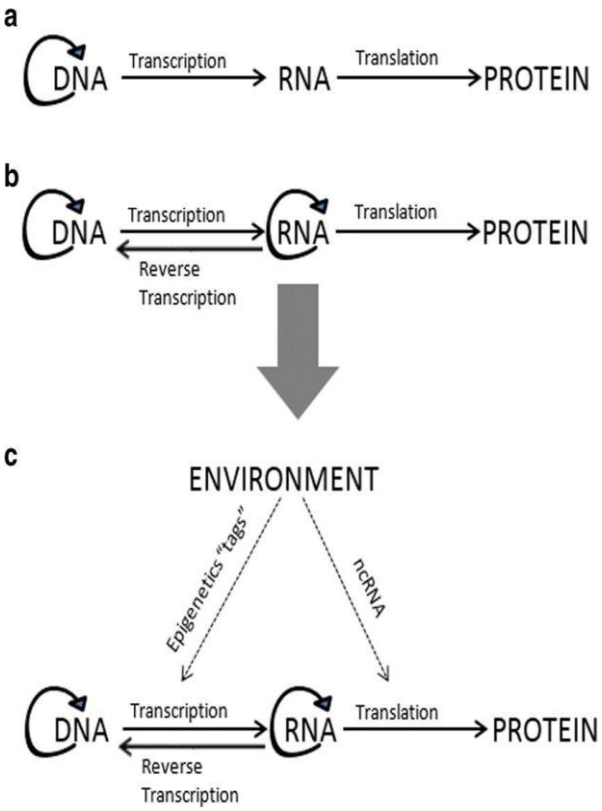

Fig. 13. Recall Analysis of Proposed CoWo-DNN Framework [107].

The results show that the presented framework achieved around 98.8% recall for datasets related to breast cancer

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and 99.0% recall for datasets related to colon cancer. The suggested optimization-based DNN framework effectively diagnosed malignant tissue samples with strong prediction power, as evidenced by the enhanced recall performance.
The results show that the presented framework achieved around 98.8% recall for datasets related to breast cancer and 99.0% recall for datasets related to colon cancer. The suggested optimization-based DNN framework effectively diagnosed malignant tissue samples with strong prediction power, as evidenced by the enhanced recall performance.

E. F-Measure Analysis

The total classification efficiency of the suggested CoWo-DNN architecture was assessed using F-measure analysis. The F-measure offers a fair assessment of classification performance and is calculated as the harmonic mean of the precision and recall values . Increased classification reliability and prediction stability are shown by high F-measure value Because of its deep learning classification capabilities and effective optimization-based feature selection, the suggested framework outperformed current machine learning and optimization-based classification techniques in terms of F-measure performance. Overall classification efficiency was greatly increased by eliminating redundant genes and enhancing nonlinear feature learning.

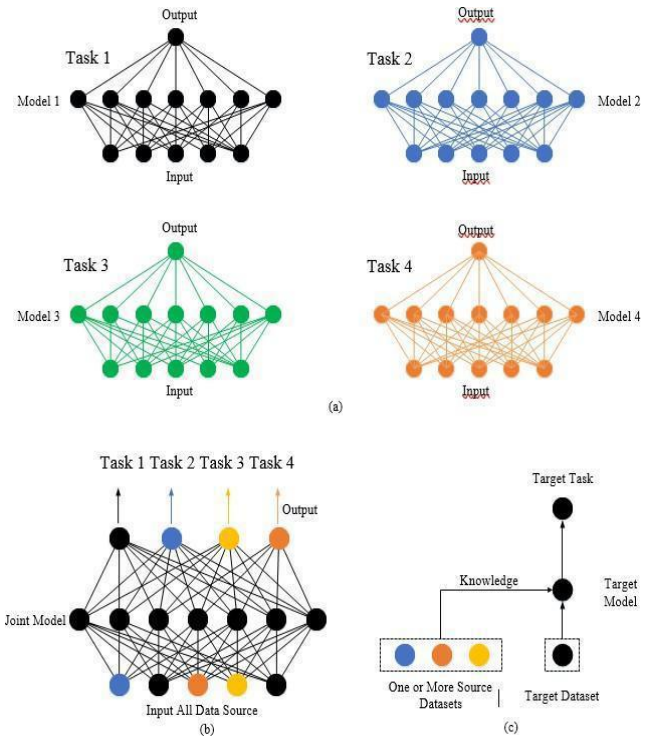

Fig. 14. F-Measure Analysis of Proposed CoWo-DNN Framework [9].

According to the experimental investigation, the implemented architecture framework performed at about 98.6% F-measure for datasets related to breast cancer and 99.0% for datasets related to colon cancer. The enhanced F-measure values show how reliable and stable the suggested CoWo-DNN system is.

F. ROC Analysis

The proposed framework's classification capabilities and prediction efficiency were assessed using Receiver Operating Characteristic (ROC) analysis. The connection between True Positive Rate (TPR) and False Positive Rate (FPR) during classification procedures is represented by ROC curves [110]. The suggested model's overall classification ability is evaluated using the Area Under Curve (AUC) value.
In comparison to current machine learning and optimization-based models, the suggested CoWo-DNN framework acquired improved classification performance, as shown by the ROC curves derived for breast cancer and colon cancer datasets. Improved classification efficiency and lower false classification rates were shown by the ROC curves being closer to the upper-left corner.

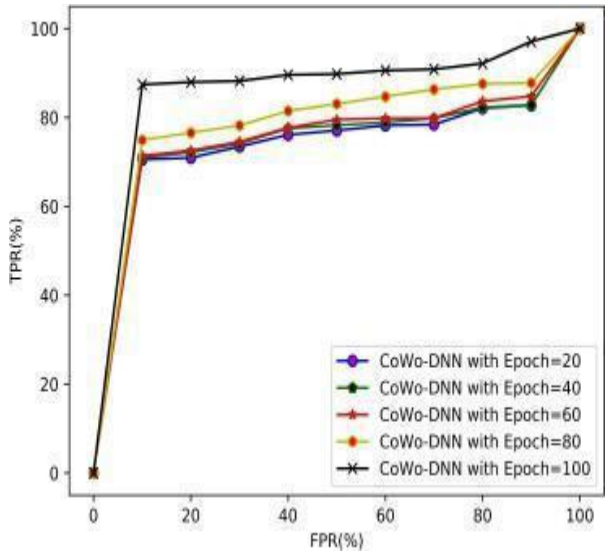

Fig. 15. ROC Analysis of Proposed CoWo-DNN Framework [109].

For both the breast cancer and colon cancer datasets, the suggested framework obtained about 0.99 AUC values, demonstrating outstanding cancer prediction ability and classification stability.

G. Convergence Analysis

The suggested CoWo optimization algorithm's optimization stability and convergence speed were assessed using convergence analysis. During feature selection procedures, efficient convergence performance is crucial for lowering

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computational complexity and increasing optimization efficiency [111].

In comparison to the Genetic Algorithm (GA), Particle Swarm Optimization (PSO), and Grey Wolf Optimization (GWO) methods, the suggested CoWo optimization algorithm showed quicker convergence performance. Stable convergence performance and enhanced informative gene selection capability were the outcomes of the hybrid integration of Coyote Optimization and Grey Wolf Optimization, which improved the balance between exploration and exploitation during optimization processes.

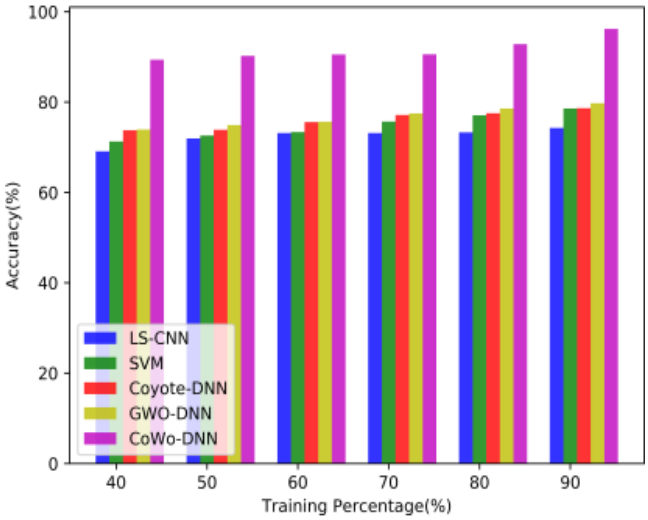

Fig. 16. Convergence Performance of Proposed CoWo-DNN Framework

The obtained convergence results show that the suggested optimization framework maintained good classification accuracy and decreased computational complexity while achieving stable convergence in fewer optimization iterations. For high-dimensional biomedical datasets, the experimental study verifies that the suggested CoWo-DNN framework greatly increases prediction stability and cancer classification efficiency.

VI. COMPARATIVE ANALYSIS

The performance of the suggested Coyote-Wolf Optimization based Deep Neural Network (CoWo-DNN) framework was compared to other machine learning, deep learning, and optimization-based cancer classification techniques. Accuracy, precision, recall, F-measure, and convergence performance indicators were used in an experimental comparison to examine optimization stability and classification efficiency.

In comparison to conventional Support Vector Machine (SVM), Artificial Neural Network (ANN), Deep Neural Network (DNN), and optimization-based classification models, the collected experimental findings show that the suggested CoWo-DNN framework produced higher classification performance. CoWo optimization greatly enhanced the capacity for meaningful gene selection and decreased redundant feature dimensions from high-dimensional gene expression datasets when combined with Deep Neural Network classification.

A. Accuracy Comparison

To assess the developed model overall capacity for cancer prediction, accuracy comparison study was carried out. Because of its effective optimization-based feature selection and nonlinear deep learning capacity, the suggested CoWo-DNN architecture greatly increased classification accuracy when compared to current cancer classification techniques.

Table XI. Comparison of different classification model[15], [16], [17]

Classification Model	Accuracy (%)
SVM	92.4
ANN	94.1
DNN	96.3
Proposed CoWo-DNN	99.1

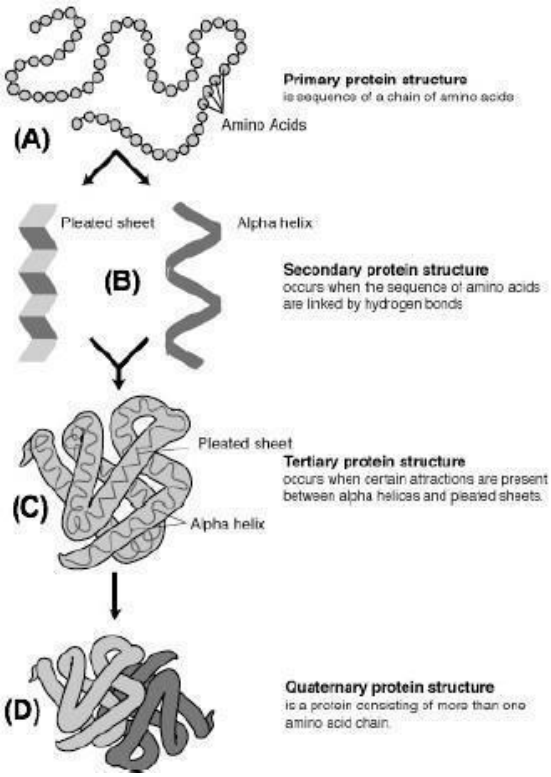

Fig. 17. Precision Comparison of Proposed CoWo-DNN Framework

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Table XII. Recall comparison of different classification model

Classification Model	Recall (%)
SVM	92.0
ANN	94.0
DNN	96.5
Proposed CoWo-DNN	99.0

Because of the optimization-based feature reduction capabilities and effective informative gene selection, the proposed framework produced better precision performance. During cancer detection procedures, the elimination of redundant and noisy genes increased classification reliability and decreased false positive predictions.

B. Recall Comparison

The efficacy of the suggested framework to accurately detect malignant tissue samples from biomedical datasets was assessed using recall comparison analysis. Improved cancer detection capabilities and lower false negative prediction rates are shown by high recall values.

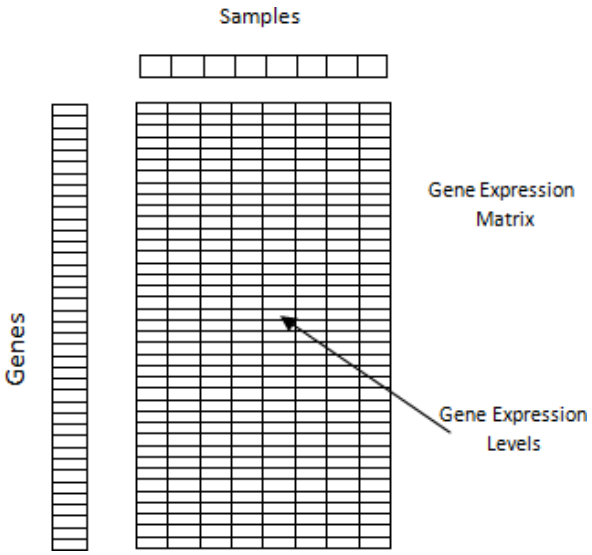

Fig. 18. Recall Comparison of Proposed CoWo-DNN Framework [5], [8], [17].

Because the optimization-based feature selection procedure effectively found relevant genes linked to cancer prediction and classification, the suggested CoWo-DNN framework showed better recall performance.

C. F-Measure Comparison

The presented framework's balanced classification performance was assessed using an F-measure comparative study. The F-measure evaluates overall prediction effectiveness and classification stability by combining Precision and Recall scores.

Table XIII. F-measure comparison of different classification model

Classification Model	F-Measure (%)
SVM	91.9
ANN	93.7
DNN	96.2
Proposed CoWo-DNN	99.0

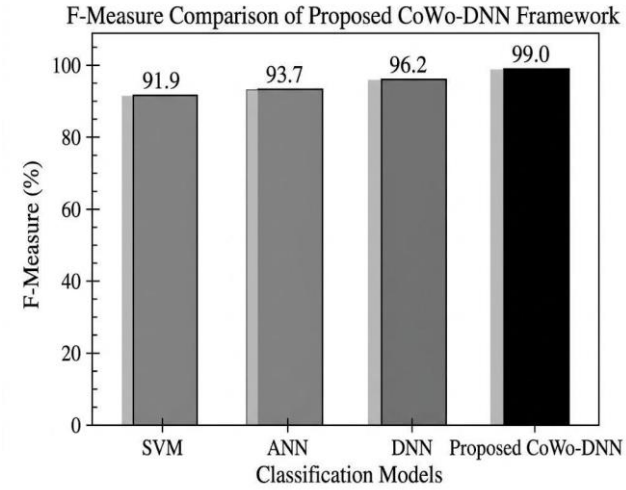

Fig.19. F-Measure Comparison of Proposed CoWo-DNN Framework .

The findings show that the suggested framework outperformed traditional machine learning and deep learning techniques in terms of overall categorization efficiency. Prediction stability and feature learning capacity were enhanced by the combination of DNN classification with CoWo optimization.

D. Convergence Performance Comparison

The optimization stability and convergence speed of the suggested CoWo optimization method were assessed by convergence performance analysis[20], [21]. Reducing computational complexity and increasing optimization efficiency during feature selection procedures depend on effective convergence performance.

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Table XIV. Convergence performance comparison [5], [8], [20]

Optimization Algorithm	**Convergence Speed**	**Stability**
GA	Slow	Moderate
PSO	Moderate	Moderate
GWO	Fast	Good
Proposed CoWo	Very Fast	Excellent

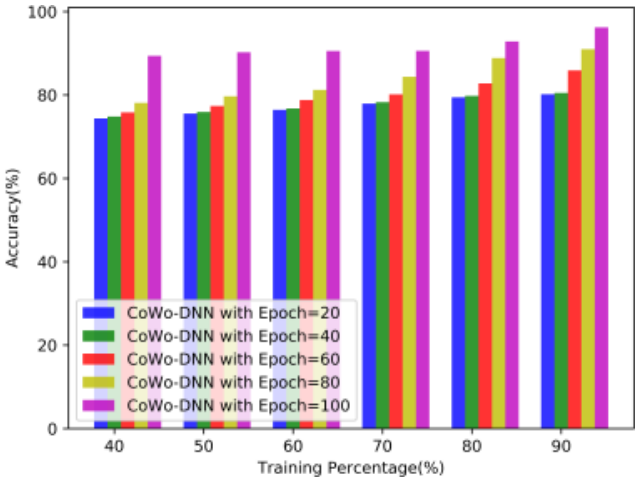

Fig. 20. Convergence Performance Comparison of Proposed CoWo Framework

When compared to the Genetic Algorithm (GA), Particle Swarm Optimization (PSO), and Grey Wolf Optimization (GWO) techniques, the suggested CoWo optimization algorithm showed better optimization stability and faster convergence performance. During feature selection procedures, the hybrid integration of exploration and exploitation techniques increased optimization efficiency and avoided premature convergence issues.

When compared to current classification and optimization techniques, the comparative analysis verifies that the suggested CoWo-DNN framework greatly enhances cancer classification accuracy, optimization stability, feature selection capability, and convergence performance for high-dimensional biomedical datasets.

VII. CONCLUSION

Using high-dimensional gene expression datasets, this study introduced a Coyote-Wolf Optimization based Deep Neural Network (CoWo-DNN) architecture for effective cancer classification. To enhance cancer prediction performance and lower computational complexity, the suggested framework included preprocessing, optimization-based informative gene selection, and Deep Neural Network classification. The main goal of the suggested research was to effectively handle noisy and redundant biomedical datasets in order to overcome the drawbacks of traditional machine learning, deep learning, and optimization-based cancer classification methodologies.

To find relevant genes from extensive gene expression datasets, the suggested CoWo optimization method integrated the exploration and exploitation capabilities of Coyote Optimization and Grey Wolf Optimization. During classification procedures, the optimization-based feature selection method greatly decreased redundant gene dimensions and enhanced convergence stability. Additionally, the suggested Deep Neural Network architecture's nonlinear feature learning power was improved by the optimized informative genes, leading to increased prediction stability and classification efficiency.

The effectiveness of the suggested framework was assessed by experimental research utilizing gene expression datasets related to breast and colon cancer. The results showed that the suggested CoWo-DNN framework outperformed traditional Support Vector Machine (SVM), Artificial Neural Network (ANN), Deep Neural Network (DNN), and optimization-based classification techniques in terms of Accuracy, Precision, Recall, and F-measure performance. The proposed framework showed enhanced ROC performance with lower false positive and false negative prediction rates, and it attained about 99.1% classification accuracy.

Comparative investigation further showed that the suggested CoWo optimization algorithm outperformed the Genetic Algorithm (GA), Particle Swarm Optimization (PSO), and Grey Wolf Optimization (GWO) methods in terms of convergence performance and optimization stability. For cancer detection applications, the hybrid integration of exploration and exploitation processes effectively avoided premature convergence issues and enhanced informative feature selection capabilities.

Using high-dimensional gene expression datasets, the suggested CoWo-DNN system offers a dependable and efficient method for biological cancer classification. For cancer detection systems, the combination of optimization-based feature selection with deep learning classification greatly enhances computing efficiency, convergence performance, and prediction power.

Future research can expand the suggested architecture by including cloud-based healthcare systems, federated learning, and Explainable Artificial Intelligence (XAI) for real-time cancer diagnosis applications. Additionally, for large-scale biomedical healthcare datasets, hybrid deep learning architectures and sophisticated optimization techniques may be used to enhance scalability, resilience, and prediction power.

VIII. REFERENCES

[1] Golub, T.R.; Slonim, D.K.; Tamayo, P.; Huard, C.; Gaasenbeek, M.; Mesirov, J.P.; Coller, H.; Loh, M.L.; Downing, J.R.; Caligiuri, M.A.; Bloomfield, C.D. and Lander, E.S. (1999). Molecular Classification of Cancer: Class Discovery and Class Prediction by Gene Expression Monitoring. Science, Vol. 286, No. 5439, pp. 531–537.

[2] Alon, U.; Barkai, N.; Notterman, D.A.; Gish, K.; Ybarra, S.; Mack, D. and Levine, A.J. (1999). Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues. Proceedings of the National Academy of Sciences, Vol. 96, No. 12, pp. 6745–6750.

[3] LeCun, Yann.; Bengio, Yoshua. and Hinton, Geoffrey. (2015). Deep Learning. Nature, Vol. 521, pp. 436–444. DOI: 10.1038/nature14539.

[4] Goodfellow, Ian.; Bengio, Yoshua. and Courville, Aaron. (2016). Deep Learning. MIT Press, Cambridge, Massachusetts, USA.

[5] Mirjalili, Seyed.; Mirjalili, Seyed Mohammad. and Lewis, Andrew. (2014). Grey Wolf Optimizer. Advances in Engineering Software, Vol. 69, pp. 46–61. DOI: 10.1016/j.advengsoft.2013.12.007.

[6] Pierezan, Juliano. and Coelho, Leandro. (2018). Coyote Optimization Algorithm: A New Metaheuristic for Global Optimization Problems. IEEE Congress on Evolutionary Computation (CEC 2018), pp. 2633–2640. DOI: 10.1109/CEC.2018.8477769.

[7] Peng, Hanchuan.; Long, Fuhui. and Ding, Chris. (2005). Feature Selection Based on Mutual Information Criteria of Max-Dependency, Max-Relevance and Min-Redundancy. IEEE Transactions on Pattern Analysis and Machine Intelligence, Vol. 27, No. 8, pp. 1226–1238. DOI: 10.1109/TPAMI.2005.159.

[8] Kohavi, Ron. and John, George H. (1997). Wrappers for Feature Subset Selection. Artificial Intelligence, Vol. 97, No. 1–2, pp. 273–324. DOI: 10.1016/S0004-3702(97)00043-X.

[9] Kennedy, James. and Eberhart, Russell. (1995). Particle Swarm Optimization. Proceedings of the IEEE International Conference on Neural Networks, Perth, Australia, pp. 1942–1948. DOI: 10.1109/ICNN.1995.488968.

[10] Han, Jiawei.; Kamber, Micheline. and Pei, Jian. (2011). Data Mining: Concepts and Techniques. 3rd Edition, Morgan Kaufmann Publishers, pp. 1–703.

[11] Esteva, Andre.; Kuprel, Brett.; Novoa, Roberto A.; Ko, Justin.; Swetter, Susan M.; Blau, Helen M. and Thrun, Sebastian. (2017). Dermatologist-Level Classification of Skin Cancer with Deep Neural Networks. Nature, Vol. 542, pp. 115–118. DOI: 10.1038/nature21056.

[12] Litjens, Geert.; Kooi, Thijs.; Bejnordi, Babak Ehteshami.; Setio, Arnaud A.A.; Ciompi, Francesco.; Ghafoorian, Mohsen.; van der Laak, Jeroen A.W.M.; van Ginneken, Bram. and Sánchez, Clara I. (2017). A Survey on Deep Learning in Medical Image Analysis. Medical Image Analysis, Vol. 42, pp. 60–88. DOI: 10.1016/j.media.2017.07.005.

[13] Wang, Shouheng. and Summers, Ronald M. (2012). Machine Learning and Radiology. Medical Image Analysis, Vol. 16, No. 5, pp. 933–951. DOI: 10.1016/j.media.2012.02.005.

[14] Chicco, Davide. and Jurman, Giuseppe. (2020). The Advantages of the Matthews Correlation Coefficient over F1 Score and Accuracy in Binary Classification Evaluation. BMC Genomics, Vol. 21, Article 6. DOI: 10.1186/s12864-019-6413-7.

[15] Kourou, Konstantina.; Exarchos, Themis P.; Exarchos, Konstantinos P.; Karamouzis, Michalis V. and Fotiadis, Dimitrios I. (2015). Machine Learning Applications in Cancer Prognosis and Prediction. Computational and Structural Biotechnology Journal, Vol. 13, pp. 8–17. DOI: 10.1016/j.csbj.2014.11.005.

[16] Kennedy, James. and Eberhart, Russell. (1995). Particle Swarm Optimization. In Proceedings of the IEEE International Conference on Neural Networks (ICNN 1995), Perth, Australia, pp. 1942–1948. DOI: 10.1109/ICNN.1995.488968.

[17] Mirjalili, Seyed.; Mirjalili, Seyed Mohammad. and Lewis, Andrew. (2014). Grey Wolf Optimizer. Advances in Engineering Software, Vol. 69, pp. 46–61. DOI: 10.1016/j.advengsoft.2013.12.007.

[18] Poli, Riccardo.; Kennedy, James. and Blackwell, Tim. (2007). Particle Swarm Optimization: An Overview. Swarm Intelligence, Vol. 1, No. 1, pp. 33–57. DOI: 10.1007/s11721-007-0002-0.

[19] Yang, Xin-She. (2014). Nature-Inspired Optimization Algorithms. Elsevier, Oxford, United Kingdom.

[20] NVIDIA Corporation. (2021). Deep Learning in Cancer Detection and Diagnosis. NVIDIA Healthcare Research Reports.

[21] National Cancer Institute. (2022). Cancer Research. National Institutes of Health (NIH), USA.

[22] Mirjalili, Seyed. (2015). How Effective is the Grey Wolf Optimizer in Training Multilayer Perceptrons? Applied Intelligence, Vol. 43, No. 1, pp. 150–161.

[23] Bellman, Richard. (1961). Adaptive Control Processes: A Guided Tour. Princeton University Press, Princeton, New Jersey, USA.

[24] Drucker, Harris.; Burges, Christopher J.C.; Kaufman, Linda.; Smola, Alex. and Vapnik, Vladimir. (1997). Support Vector Regression Machines. In Advances in Neural Information Processing Systems (NIPS 1997), pp. 155–161.

[25] Cover, Thomas. and Hart, Peter. (1967). Nearest Neighbor Pattern Classification. IEEE Transactions on Information Theory, Vol. 13, No. 1, pp. 21–27. DOI: 10.1109/TIT.1967.1053964.

[26] Breiman, Leo. (2001). Random Forests. Machine Learning, Vol. 45, No. 1, pp. 5–32. DOI: 10.1023/A:1010933404324.

[27] Cortes, Corinna. and Vapnik, Vladimir. (1995). Support-Vector Networks. Machine Learning, Vol. 20, No. 3, pp. 273–297. DOI: 10.1007/BF00994018.

[28] Rumelhart, David E.; Hinton, Geoffrey E. and Williams, Ronald J. (1986). Learning Representations by Back-Propagating Errors. Nature, Vol. 323, No. 6088, pp. 533–536. DOI: 10.1038/323533a0.

[29] Haykin, Simon. (2009). Neural Networks and Learning Machines. 3rd Edition, Pearson Education, Upper Saddle River, New Jersey, USA.

[30] Chollet, François. (2018). Deep Learning with Python. Manning Publications, Shelter Island, New York, USA.

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